

SEARCH REQUEST FORM

61346

Requestor's Name: Jeanine Goldberg Serial Number: 09/619643
Date: 2/28/02 Phone: 306-5817 Art Unit: 1634

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

Granbank AI978199 } translate in 6 frames
AI734448

Seq 5 - translate in 6 frames

compare resulting proteins

Point of Contact:
Barb O'Brien
Technical Information Specialist
STIC CM1 6A05 308-4291

STAFF USE ONLY

Date completed: 2-28-02
Searcher: 1205
Terminal time: 20
Elapsed time: plus 18
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site
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Vendors
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GCG Other

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TOIG OF: ai734448 check: 6406 from: 1 to: 582
LOCUS      AI734448      582 bp      mRNA      EST      02-FEB-2000
DEFINITION 606031E07.x1 606 - Ear tissue cDNA library from Schmidt lab Zea
ACCESSION  AI734448
VERSION    AI734448.1 GI:5055561
KEYWORDS   EST.
SOURCE     Zea mays.
ORGANISM   Zea mays.
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            Clad3; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 582)
AUTHORS   Walbot V.
TITLE      Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL    Unpublished (1999)
COMMENT    Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 606031 row: E column: 07.
FEATURES   Location/Qualifiers
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             /organism="Zea mays"
             /cultivar="Ohio43"
             /db_xref="taxon:4577"
             /clone_id="606 - Ear tissue cDNA library from Schmidt
             lab"
             /tissue_type="mixed"
             /dev_stage="ear length from 0.5 cm - 2.0 cm"
             /lab_host="XLOLR (Stratagene)"
             /note="Organ: Immature ear; Vector: pBK-CMV; Site_1: EcoRI
             /Site_2: XhoI; Mixed ear tissue cDNA library from Schmidt
             lab"
BASE COUNT 158 a 131 c 122 g 170 t 1 others
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TOIG OF: ai978199 check: 48 from: 1 to: 442
LOCUS      AI978199      442 bp      mRNA      EST      27-AUG-1999
DEFINITION 614041D10.x2 614 - root cDNA library from Walbot Lab Zea mays cDNA.
ACCESSION  AI978199
VERSION    AI978199.1 GI:5791407
KEYWORDS   EST.
SOURCE     Zea mays.
ORGANISM   Zea mays.
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            Clad3; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 442)
AUTHORS   Walbot V.
TITLE      Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL    Unpublished (1999)
COMMENT    Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 614041 row: D column: 10.
FEATURES   Location/Qualifiers
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             /organism="Zea mays"
             /cultivar="W23"
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             /clone_id="614 - root cDNA library from Walbot Lab"
             /tissue_type="root"
             /dev_stage="3-4 days old"
             /lab_host="XLOLR"
             /note="Organ: root; Vector: pBluescriptII SK+; Site_1:
             /EcoRI; Site_2: XhoI; 3-4 days old root tissue from Walbot
             lab (LM)"
BASE COUNT 126 a 107 c 93 g 116 t
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      80      90      100      110      120      130      140
SWQDISKLTGTEFLIIFYCCLGKLIACKVHCKSRNPPEAGDRALEKPEKMTLVSDGQDYHLHRHMCAGRS
      80      90      100      110      120      130      140
GLEMAYXYTLIHEKS
PG
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10. SEQ-5.2 (1-110)
A1978199_2

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Initial Score = 10 Optimized Score = 53 Significance = -0.51
Residue Identity = 11% Matches = 13 Mismatches = 91
Gaps = 0 Conservative Substitutions = 6

X      10      20      30      40      50      60      70
DNLVHPMKRGSTWALXGRDPRLLLDSSWSNELCRLXACQGNDRKREKFOXYNTRDLAKKAVINHATFLF
      10      20      30      40      50      60      70
TKOYSCPIQOKNNSSMCLCPALFSCVNYTAISRPGNVIPIKIKROMFCFSATWTOKXKKVAMLITA
X      10      20      30      40      50      60      70
      80      90      100      110      120      130      140
YFWVHVAEKQONICLFILIGITFPXGLEMAVXYTLIHEKS
      80      90      100      110      120      130      140
FLARSLVLTWVNFSLSLPSWQASHLOSILQEQSRSGGSRPRACQVDPDRFOGWTRLSSAXTLVCLGQ
SW

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11. SEQ-5.2 (1-110)
A1734448_3

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Initial Score = 10 Optimized Score = 42 Significance = -0.51
Residue Identity = 9% Matches = 10 Mismatches = 99
Gaps = 0 Conservative Substitutions = 1

      40      50      60      70      80      90      100
KGAVLSKRTTAPACASVLYHFSHWVYTIQPSQPTGMXFPISKKGCSVASLQHPKMKIKKLHGXSLSW
      40      50      60      70      80      90      100
      110      120      130      140      150      160      170
LDDSSWSNELCRLXACQGNDRKREKFOXYNTRDLAKKAVINHATFLFYPFWVHVAEKQONICLFILIGITF
      110      120      130      140      150      160      170
ODLSGXLTGILIFLYHCLGLLIACKVHCKSRNPPEAGDRALEKPEKMTLVSDGQDYHLHRHMMWAMRGRRH
      100      110      120      130      140      150      160      170
      180      190
PXGLEMAVXYTLIHEKS
      180      190
PXLHRVKGGRGHYCRKSS
      180      190

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12. SEQ-5.2 (1-110)
A1734448_2

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Initial Score = 10 Optimized Score = 52 Significance = -0.51
Residue Identity = 11% Matches = 13 Mismatches = 91
Gaps = 0 Conservative Substitutions = 6

X      10      20      30      40
DNLVHPMKRGSTWALXGRDPRLLLDSSWSNELCRLXACQEG
      10      20      30      40
FFFFFFFFFFSKFTSGLTRKAMDHRITTKGSCPIQOKNNSSMCLCPALFSCVNYTAISRPGNVIPI
      10      20      30      40      50      60      70

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      50      60      70      80      90      100
NDKREKREKFOXYNTRDLAKKAVINHATFLFYPFWVHVAEKQONICLFILIGITFPXGLEMAVXYTLIHEKS
      80      90      100      110      120      130      140
NKKROMFCFSATWTOKXKKVAMLITAFILARSLVLTWVNFSLSLPSWQASHLOSILQEQSRSGG
      150      160      170      180      190
RPRKAGDPRFOGWTRLSSAXTLVGLGQASSXSXSRRQREGSLLPQ

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Residue Identity ~ 8% Matches ~ 9 Mismatches ~ 92
Gaps ~ 0 Conservative Substitutions ~ 8

TRAPPGTAVSMOMITLILGNGSPGLGKAIPEFFWIAPLGAMNFAGYELKKAMIDEKSSSESTREIL
10 20 30 40 50 60 70
TFLMXCILYSHLKAALRECNQYOKKADYLLLLCNMDPKIKKXSCWVDHCFLGKIS

RVLSLEFFSSFIATFLASSXPAKFIAPRGAIQKKPGIAPLKSPPSPPRMDKI
60 70 80 90 100 X
PRKQXSTMQLFYIFGSMLORSNRTSAFFXYWELHSRRALRWLSIHYMKVLEDEGTCSCSFAGXDSL
80 90 100 110 120 X 130 140

VL

4. SEQ-5_6 (1-109)
AI97819_5

Initial Score ~ 16 Optimized Score ~ 47 Significance ~ -0.35
Residue Identity ~ 12% Matches ~ 14 Mismatches ~ 88
Gaps ~ 1 Conservative Substitutions ~ 6

SGGLAIVTPPEVDVKKRMMPAPGPPVSMOMITLILGNGSPGLGKAIPEFFWIAPLGAMNFAGYELAK
X 10 20 30 40 50 60 70
TFLMXCILYSHLKAALRECNQYOKKADYLLLLCNMDPKIKKXSCWVDHCFLGKISRVDSLEFFSSFI

KIRKXSCWVDHCFLGKISRVDSLEFFSSFIATFLASSXPAKFIAPRGAIQKKPGIAPLKSPPSPPRMDKI
40 50 60 70 80 90 100 X
AKKAVINHAFTLEFYFWVHVAEKOONICFLILGITPPXGLE-MAVXYTTLHEKSAAGORHMLLELFPQWIGQL
80 90 100 110 120 130 140 X

TCF

5. SEQ-5_6 (1-109)
AI734448_5

Initial Score ~ 16 Optimized Score ~ 47 Significance ~ -0.35
Residue Identity ~ 6% Matches ~ 7 Mismatches ~ 96
Gaps ~ 0 Conservative Substitutions ~ 6

SGGLAIVTPPEVDVKKRMMPAPGPPVSMOMITLILGNGSPGLGKAIPEFFWIAPLGAMNFAGYELAK
X 10 20 30 40 50 60 70
TFLMXCILYSHLKAALRECNQYOKKADYLLLLCNMDPKIKKXSCWVDHCFLGKISRVDSLEFFSSFI

IIAFLASSXPAKFIAPRGAIQKKPGIAPLKSPPSPPRMDKI
70 80 90 100 X
KAMIDEKSSSESTREILPRKQXSTMQLFYIFGSMLORSNRTSAFFXYWELHSRRALRWLSIHYMKVLE
80 90 100 110 X 120 130 140

DRGTCWSCSFAGXDSLVL
150 160

6. SEQ-5_6 (1-109)
AI734448_4

Initial Score ~ 16 Optimized Score ~ 48 Significance ~ -0.35
Residue Identity ~ 12% Matches ~ 17 Mismatches ~ 87
Gaps ~ 26 Conservative Substitutions ~ 5

X 10 20

TCGNSDPSLXRDDEXDADCPSPPTSVYADDNLVHPMKKCSPMALXGRDPLLLIDCSSWSNELCRLXACQCGN
10 20 30 40 50 60 70
TFLMXCILYSHLKAALRECNQY

OKKADYLLLLCNMDPKIKKXSCWVDHCFLGKISRVDSLEFFSSFIATFLASSXPAKFIAPRGAIQKKP-
10 20 30 40 50 60 70 80 90
DKRXXRFQXVNTFRDLAKKAVINHAFTLEFYFWVHVAEKOONICFLILGITPPXGLEMAVXYTTLHEKSAAGOR
30 40 50 60 70 80 90 100 110 120 130 140

-----GIAPLKSPPSPPRMDKI X
HMLELLEFCWIGOLPCEVIRKXSIATFLVDPVNLKXKKKKKKKK
150 160 170 180 190

7. SEQ-5_6 (1-109)
AI734448_3

Initial Score ~ 14 Optimized Score ~ 41 Significance ~ -0.41
Residue Identity ~ 7% Matches ~ 8 Mismatches ~ 83
Gaps ~ 5 Conservative Substitutions ~ 7

TFLMXCILYSHLKAALRECNQYOKKADYLLLLCNMDPKIKKXSCWVDHCFLGKISRVDSLEFFSSFIATFLA
X 10 20 30 40 50 60 70
FFFFFFFFFFFRANLHRVXOCRLWIIIGXONKGAIVLSK-----RTIAPACASVXLHFHVMVTIO
X 10 20 30 40 50 60

SSXPAKFIAPRGAIQKKPGIAPLKSPPSPPRMDKI
80 90 100 X
PSGPGPMGXPPISKKGCSVASIQHGPKNKIKKLHGKSLSMODLSCLTLGITLPIYHCLLKGKLYACVHS
70 80 90 100 110 120 130

KFSNPEAGDRAIKE
140

8. SEQ-5_6 (1-109)
AI734448_2

Initial Score ~ 14 Optimized Score ~ 46 Significance ~ -0.41
Residue Identity ~ 5% Matches ~ 6 Mismatches ~ 93
Gaps ~ 0 Conservative Substitutions ~ 10

TFLMXCILYSHLKAALRECNQYOKKADYLLLLCNMDPKIKKXSCWVDHCFLGKISRVDSLEFFSSFI
X 10 20 30 40 50 60 70
FPPPPFFFFFXXSKFTSGLWRKAMDHRRTIKGSCPTQOKNNSSMCPLALFSCNVYVTAISRFGVIVP
X 10 20 30 40 50 60 70

FLVSSXPAKFIAPRGAIQKKPGIAPLKSPPSPPRMDKI
70 80 90 100 X
NIKXROMPCFCEFAFTQKXNKKVAMLTITAFIARSVLVLTWNFSLSLSPSWAHSLOSSLDEQSRSGGS
80 90 100 110 X 120 130 140

RPXVAGDPRFQGTIRLS
150 160

9. SEQ-5_6 (1-109)
AI97819_3

Initial Score ~ 11 Optimized Score ~ 32 Significance ~ -0.49
Residue Identity ~ 11% Matches ~ 8 Mismatches ~ 59
Gaps ~ 0 Conservative Substitutions ~ 3

TFLMXCILYSHLKAALRECNQYOKKADYLLLLCNMDPKIKKXSCWVDHCFLGKISRVDSLEFFSSFIATFLA
10 20 30 40 50 60 70


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      80      90      100      X      ONKXAVLSKRRTAPACASVLFHFSHWYTIOD
      |      |      |      |      |
SSXPAKFTAPRGAIQKKPGIAPLKSPSGSPFPMMDKI      X
      |      |      |      |      |
SOGPTGMXFPISKGRCSVASLHGPPNKKTKKLHGXSLSLMDQSLXLTGIFLFIYHCLGLKIACKVCSK
      40      50      60      70      80      90      100
      |      |      |      |      |
RSNPPEACGRALKPEP
      110      120

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10. SEQ-5_6 (1-109)
AI978199_2

Initial Score	-	11	Optimized Score	-	42	Significance	-	-0.49
Residue Identity	-	9%	Matches	-	10	Mismatches	-	87
Gaps	-	0	Conservative Substitutions	-			-	6

[illegible]

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11. SEQ-5-6 (1-109)
AI978199_4

Initial Score	=	11	Optimized Score	=	48	Significance	=	-0.49
Residue Identity	=	128	Matches	=	16	Mismatches	=	81
Gaps	=	15	Conservative Substitutions				=	12

X 10 20 30 40 50
 TELMXCIILSHLKALRECSNQYQKKAADVLLLCNMDDPRKKKSCSMVHCELGKII
 | : : : : :
 APGLPLAHQCLCRXKSCPSLEIRVHLGSRANSPASSGLILEQXTLLDAMSLPRRQKKMKRIPVCSHERNS
 10 20 30 40 50 60 70

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60      70      80      90     100
SVRVLEFFSSFIATLASSXPAKFIAPGAIQKKGIAP-----LKSSGSPFPRMDKI
      |      |      |      |      |      |      |      |      |
      |      |      |      |      |      |      |      |      |
      |      |      |      |      |      |      |      |      |
COSSDPCNFILFLFPCPCREATEHIHPFDIGNYIPVPGXDCIYITFXKCKPTEATAGANVLLDRTAAH
      80      90      100     110     120     130     140
LFQ

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12. SEQ-5_6 (1-109)
A1734448_6

Initial Score	=	11	Optimized Score	=	48	Significance	=	-0.49
Residue Identity	=	12%	Matches	=	16	Mismatches	=	81
Gaps	=	15	Conservative Substitutions				=	12

	10	20	30
X			
FLMXCILYSHLALRECN			
SQYQKADVLLLCNMDP			
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[illegible]

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LSSPSGPFPRMDKI

TEAHAGAVLLLDRTAPLECYPPMIHSLPCXTRCKFALKKKKKKKKKKK
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Thu Feb 28 15:47:36 2002

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file seq-5_4.res made by bobryen on Thu 28 Feb 102 15:46:18 -PST.

Query sequence being compared: SEQ-5_4 (1-111)
Number of sequences searched: 12
Number of scores above cutoff: 12

Results of the initial comparison of SEQ-5_4 (1-111) with:
File: genbanktrans.pep

Seq 5, translation frame 4

```

N 100-
U 50-
M 50-
B 50-
E 50-
R 50-
O 10-
F 10-
S 5-
E 5-
Q 5-
U 5-
E 5-
N 5-
C 5-
E 5-
S 5-
SCORE 0 112 24 37 49 61 73 86 98 110
STDEV 0 1 1 1 1 1 1 1 1 1

```

PARAMETERS

Similarity matrix PAM-150 K-tuple 1
Threshold level of sim. 16%
Mismatch penalty 1 Joining penalty 20
Gap penalty 5.00 Window size 109
Gap size penalty 0.05
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean 28 Median 13 Standard Deviation 38.34
Times: CPU 00:00:00.00 Total Elapsed 00:00:01.00
Number of residues: 2036
Number of sequences searched: 12
Number of scores above cutoff: 12

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt.	Sign.	Frame
1. A1978199_2	**** 2 standard deviations above mean ****	146	110	110	2.14	0
2. A1734448_2	**** 2 standard deviations above mean ****	193	110	110	2.14	0
3. A1978199_1	TOIG of: a1978199 check: 48	147	17	47	-0.29	0
4. A1978199_6	TOIG of: a1978199 check: 48	146	13	48	-0.39	0
5. A1734448_5	TOIG of: a1734448 check: 640	193	13	48	-0.39	0
6. A1734448_1	TOIG of: a1734448 check: 640	194	13	53	-0.39	0
7. A1978199_4	TOIG of: a1734448 check: 640	147	12	44	-0.42	0
8. A1734448_4	TOIG of: a1734448 check: 640	194	12	39	-0.42	0
9. A1734448_6	TOIG of: a1734448 check: 640	192	11	46	-0.44	0
10. A1978199_5	TOIG of: a1734448 check: 640	146	10	52	-0.47	0
11. A1978199_3	TOIG of: a1734448 check: 640	146	8	50	-0.52	0
12. A1734448_3	TOIG of: a1734448 check: 640	192	8	18	-0.52	0

1. SEQ-5_4 (1-111)
A1978199_2
Initial Score = 110 Optimized Score = 110 Significance = 2.14
Residue Identity = 98% Matches = 110 Mismatches = 1
Gaps = 0 Conservative Substitutions = 0

FLARSLVLTTHNMFSLSLPSWQASHLSSLOEQRSGSRXRAQVPPROGWTLS
FLARSLVLTTHNMFSLSLPSWQASHLSSLOEQRSGSRXRAQVPPROGWTLSAXTVLCLEGO
TRQVSCPIQKNNSSMCPLCLAFSCVNYTTAISRPYGNVPIPKKROMCFCSATYTOXKXNKVAMLTIA
10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200

2. SEQ-5_4 (1-111)
A1734448_2
Initial Score = 110 Optimized Score = 110 Significance = 2.14
Residue Identity = 98% Matches = 109 Mismatches = 2
Gaps = 0 Conservative Substitutions = 0

FFPPPPPPFFSKFTSGITRKAMDHRTTKGSCPIQKNNSSMCPLCLAFSCVNYTTAISRPYGNVPI
10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200
EXKRMPCCFSATYTOXKXNKVAMLTIAFLARSLVLTTHNMFSLSLPSWQASHLSSLOEQRSGSR
IRKQMFCCFSATYTOXKXNKVAMLTIAFLARSLVLTTHNMFSLSLPSWQASHLSSLOEQRSGSR
100 110 120 130 140 150 160 170 180 190 200
PXAQGDPRFQGWTRLSAXTVLCLEGOASSXSSROREGSLPQVLO
150 160 170 180 190

3. SEQ-5_4 (1-111)
A1978199_1 TOIG of: a1978199 check: 48 from: 1 to: 442
Initial Score = 17 Optimized Score = 47 Significance = -

Residue Identity ~ 10% Matches ~ 12 Mismatches ~ 93
Gaps ~ 9 Conservative Substitutions ~ 5

X
ALFSCNYYTTAISRPYGNVPIKRRQMFCFSATWTOKXKKVAMLTAFIARSLVLTTHMFS-----
NKTSELSPAKEQOLQVPLSSSTFLMKCILYSHLKALRECSOYOKKADVLLLCNMDPKIKKXSCVNDH
X 10 20 30 40 50 60 70

-HLTSLPSWQAHSLQSSLLQEOSSRRSGSRPRXRAQVDPFRQGWTRLS X
CFLGKISRVDLSLEFFSSFLIAFLASSXPAKFIAPRGATOKKGIAPLASPSGSPFRMDKIITCITDGVPGG
80 90 100 110 120 130 140

AVLV

4. SEQ-5_4 (1-111) A1978199_6

Initial Score ~ 13 Optimized Score ~ 48 Significance ~ -0.39
Residue Identity ~ 9% Matches ~ 11 Mismatches ~ 97
Gaps ~ 0 Conservative Substitutions ~ 3

X
ALFSCNYYTTAISRPYGNVPIKRRQMFCFSATWTQ
TRTAPGTPVSMOMIILICNEGLPLGFKGAIPRFFIAPLGAMNFAGYELAKKAMIKDKNSESETRLL
10 20 30 40 50 60 70

40 50 60 70 80 90 100 110
KXNKKVAMLTAFIARSLVLTTHMFSHLISLPWQAHSLQSSLLQEOSSRRSGSRPRXRAQVDPFRQGWTRL
PRXOXSTWQLFFYFEGSMLORSNRTSAFFXYWELSHRRALRWLYSIHYMKRVLEDRGTCWSCCSFAGXDSSL
80 90 100 110 120 130 140

X
S
VL
X

5. SEQ-5_4 (1-111) A1734448_5

Initial Score ~ 13 Optimized Score ~ 48 Significance ~ -0.39
Residue Identity ~ 9% Matches ~ 11 Mismatches ~ 97
Gaps ~ 0 Conservative Substitutions ~ 3

X
ALFSCNYYTTAISRPYGNVPIPN
GLAAIVTPPEVDKXHMMPAPGPPPVSMOMIILICNEGLPLGFKGAIPRFFIAPLGAMNFAGYELAKKA
10 20 30 40 50 60 70

30 40 50 60 70 80 90
IKRRQMFCFSATWTOKXKKVAMLTAFIARSLVLTTHMFSHLISLPWQAHSLQSSLLQEOSSRRSGSR
MIKDKNSESESTREILPRKXOSTWQLFFYFEGSMLORSNRTSAFFXYWELSHRRALRWLYSIHYMKRVLEDR
80 90 100 110 120 130 140

100 110
PKRAQVDPFRQGWTRLS
GTCWSCCSFAGXDSSLVLLSADDPXPSTLNPXKICSKKKKKKKKKKK
150 160 X 170 180 190

6. SEQ-5_4 (1-111)
A1734448_1 TOIG of: a1734448 check: 6406 from: 1 to: 582

Initial Score ~ 13 Optimized Score ~ 53 Significance ~ -0.39
Residue Identity ~ 10% Matches ~ 12 Mismatches ~ 88
Gaps ~ 0 Conservative Substitutions ~ 11

FEFFFEFFFEQIYIGFKKEGYSADNKTRELSPAKEQOLQVPLSSSTFLMKCILYSHLKALRECSNQ
10 20 30 40 50 X 60 70
X
ALFSCNYYTTAISRPYGNVPIPN
IKRRQMFCFSATWTOKXKKVAMLTAFIARSLVLTTHMFSHLISLPWQAHSLQSSLLQEOSSRRSGSR
100 110 120 130 140
YOKXADVLLLCNMDPKIKKXSCVNDHCFGLGKISRVDLSLEFFSSFLIAFLASSXPAKFIAPRGATOKKRGIA

100 110
PKRAQVDPFRQGWTRLS
PLKSPRGSPFRMDKIITCITDGVPGGAGIILXFTTSKGVTTIASPPD
130 160 X 170 180 190

7. SEQ-5_4 (1-111) A1978199_4

Initial Score ~ 12 Optimized Score ~ 44 Significance ~ -0.42
Residue Identity ~ 4% Matches ~ 5 Mismatches ~ 96
Gaps ~ 0 Conservative Substitutions ~ 5

X 10 20 30 40 50 60 70
ALFSCNYYTTAISRPYGNVPIKRRQMFCFSATWTOKXKKVAMLTAFIARSLVLTTHMFSHLISLPW
ARGLPLQAHQCCLCRXXSCPSLETRVHLGSLRARSPASSGLLLEOXTLQAMSLPRXOXKKMKRIPVS
X 10 20 30 40 50 60

80 90 100 110
QAHSLQSSLLQEOSSRRSGSRPRXRAQVDPFRQGWTRLS
QHEISCOESSDQPCNFFITLPLGPCREATEHLPPFDIGNVIIPVGPDGCIYITXKRCXRTAHAGAVLL
70 80 90 100 110 120 130

DK7AHLCF 140

8. SEQ-5_4 (1-111) A1734448_4

Initial Score ~ 12 Optimized Score ~ 39 Significance ~ -0.42
Residue Identity ~ 11% Matches ~ 10 Mismatches ~ 73
Gaps ~ 0 Conservative Substitutions ~ 6

10 20 X 30 40 50 60 70
ALFSCNYYTTAISRPYGNVPIPNIKRRQMFCFSATWTOKXKKVAMLTAFIARSLVLTTHMFSHLISLPW
VMRTCGNSDPSLXDEXXDDACPSRPTSVYADNDLVHPMKRGSPWALGR
X 10 20 30 40 50

80 90 100
QAHSLQSSLLQEOSSRRSGSRPRXRAQVDPFRQGWTRLS X
DPELLDCCSWSNELCRAXACQCGNDRKREKFOXYVTRDLAKKAVINHAFTLFFYVWVAEKOONICFLIL
60 70 80 90 100 110 120

G11PXYGLEMAVYVTLH
130

9. SEQ-5_4 (1-111) A1734448_6

Initial Score = 11 Optimized Score = 46 Significance = -0.44
Residue Identity = 9% Matches = 11 Mismatches = 93
Gaps = 0 Conservative Substitutions = 7

X 10 20 30 40 50 60 70
ALFSCNYYTAISRPGNVIPNPKKROMFCCFSATWTOKXNKVAMLTALARSVLVTHNFSHLSPS
LEDLRQXXPLPLTXXLXCLPLAHQCLCRXXSCPSETRVPLGSLNARSPPASSGLLLEQXTPLQAMSLPR
X 10 20 30 40 50 60 70

80 90 100 110
WQAHSLQSSLLQEOSSRSRSGSRPRAYDPRFGQWTRL
FOXXMRKIPVSOHERSCQESSDPCNFILFLGSCREATEHLEPFIDIGNYIPVGPXDCIYITXKXMR
80 90 100 110 X 120 130 140

TEAHGAVVLLDRTAPL
150 160

10. SEO-5_4 (1-111)
AI978199_5

Initial Score = 10 Optimized Score = 52 Significance = -0.47
Residue Identity = 13% Matches = 15 Mismatches = 90
Gaps = 0 Conservative Substitutions = 6

X 10 20 30
ALFSCNYYTAISRPGNVIPNPKKROMFCCFSATWT
HODCPRIYSYADDNLVHPWKRGSSTWALXGRDPLLDCCSSWSNELCRXACQEGNDKRXEKFQXVNTDL
10 20 30 X 40 50 60 70

40 50 60 70 80 90 100
OKXNKKVAMLTALARSVLVTHNFSHLSPSWQAHSLQSSLLQEOSSRSRSGSRPRAYDPRFGQWTRL
AKKAVINATLEFVHWVAEKQONICFLGITEPPXGLEMAVYTTLEHKSARQRMLELLFFCWIGOLT
80 90 100 110 120 130 140

110
LS
CF
X

11. SEO-5_4 (1-111)
AI978199_3

Initial Score = 8 Optimized Score = 50 Significance = -0.52
Residue Identity = 15% Matches = 18 Mismatches = 86
Gaps = 7 Conservative Substitutions = 7

X 10 20 30 40 50
ALFSCNYYTAISRPGNVIPNPKKROMFCCFSATWTOKXNKVAMLTALARSVLV
ONKXAVLSKRTTAPACASVLNHFHVMYTTIOPSQPTGMXPPIISKGCSVASLOHGPKNKIKKLHGXSLL
10 20 30 40 50 60 70

60 70 80 90 100 110
LTHNMFSHLSLPSWQAHSLQSSLLQEOSSRSRSGSRPRAYDPRFGQWTRL
SMODLSCLTGTGIFLIFYHCLLKLACKVHCGRSNPEEAGDRALKEPKGTIVSKDGODYHLHRHNCAMRGS
80 90 100 110 120 130 140

PG

12. SEO-5_4 (1-111)
AI734448_3

Initial Score = 8 Optimized Score = 18 Significance = -0.52

Residue Identity = 1% Matches = 1 Mismatches = 45
Gaps = 0 Conservative Substitutions = 5

X 10 20
ALFSCNYYTAISRPGNVIPN
IKRLGXSLLSMODLSCLTGTGIFLIFYHCLLKLACKVHCGRSNPEEAGDRALKEPKGTIVSKDGODYHL
100 110 120 130 140 X 150 160

30 40 50 60 70 80 90
IKKROMFCCFSATWTOKXNKVAMLTALARSVLVTHNFSHLSPSWQAHSLQSSLLQEOSSRSRSGSR
HRHMAWGRGHHPLHNVKRGHGCRRSS
170 180 190 X

100
PYRAOVD

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IntelliGenetics

FastDB - Fast Pairwise Comparison of Sequences

Release 5.4

Results file seq-5_2.res made by bobryen on Thu 28 Feb 102 15:45:27-PST.

Query sequence being compared:	SEQ-5_2 (1-110)
Number of sequences searched:	12
Number of scores above cutoff:	12

Results of the initial comparison of SEQ-5_2 (1-110) with
File : genbanktrans.pep

Seg 5, translation frame 2

PARAMETERS

Similarity matrix	PAM-150	K-tuple	1
Threshold level of sim.	16%		
Mismatch penalty	1	Joining penalty	200
Gap penalty	5.00	Window size	110
Gap size penalty	0.05		
Cutoff score	1		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	30	15	27.10

Times:	CPU	Total Elapsed
1	0.00	0.00
2	0.00	0.00
3	0.00	0.00
4	0.00	0.00
5	0.00	0.00
6	0.00	0.00
7	0.00	0.00
8	0.00	0.00
9	0.00	0.00
10	0.00	0.00
11	0.00	0.00
12	0.00	0.00
13	0.00	0.00
14	0.00	0.00
15	0.00	0.00
16	0.00	0.00
17	0.00	0.00
18	0.00	0.00
19	0.00	0.00
20	0.00	0.00
21	0.00	0.00
22	0.00	0.00
23	0.00	0.00
24	0.00	0.00
25	0.00	0.00
26	0.00	0.00
27	0.00	0.00
28	0.00	0.00
29	0.00	0.00
30	0.00	0.00
31	0.00	0.00
32	0.00	0.00
33	0.00	0.00
34	0.00	0.00
35	0.00	0.00
36	0.00	0.00
37	0.00	0.00
38	0.00	0.00
39	0.00	0.00
40	0.00	0.00
41	0.00	0.00
42	0.00	0.00
43	0.00	0.00
44	0.00	0.00
45	0.00	0.00
46	0.00	0.00
47	0.00	0.00
48	0.00	0.00
49	0.00	0.00
50	0.00	0.00
51	0.00	0.00
52	0.00	0.00
53	0.00	0.00
54	0.00	0.00
55	0.00	0.00
56	0.00	0.00
57	0.00	0.00
58	0.00	0.00
59	0.00	0.00
60	0.00	0.00
61	0.00	0.00
62	0.00	0.00
63	0.00	0.00
64	0.00	0.00
65	0.00	0.00
66	0.00	0.00
67	0.00	0.00
68	0.00	0.00
69	0.00	0.00
70	0.00	0.00
71	0.00	0.00
72	0.00	0.00
73	0.00	0.00
74	0.00	0.00
75	0.00	0.00
76	0.00	0.00
77	0.00	0.00
78	0.00	0.00
79	0.00	0.00
80	0.00	0.00
81	0.00	0.00
82	0.00	0.00
83	0.00	0.00
84	0.00	0.00
85	0.00	0.00
86	0.00	0.00
87	0.00	0.00
88	0.00	0.00
89	0.00	0.00
90	0.00	0.00
91	0.00	0.00
92	0.00	0.00
93	0.00	0.00
94	0.00	0.00
95	0.00	0.00
96	0.00	0.00
97	0.00	0.00
98	0.00	0.00
99	0.00	0.00
100	0.00	0.00

00:00:00:00

Total Elapsed
00:00:00.00

Number of residues: 2036

```
Number of sequences searched: 12
Number of scores above cutoff: 12
```

The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Init.	Opt.	length	score	Sig.	Frame

1. A1978199_5	translation frame	146	109	109	2.14	0
2. A1734448_4		194	109	109	2.14	0
**** 0 standard deviation from mean ****						

	TOIG OF: a1978199	check: 48	TOIG OF: a1734448	check: 640
3. A1734448-5	193	20	49	-0.24
4. A1978199-6	147	18	49	-0.29
5. A1978199-1	146	15	50	-0.37
6. A1734448-1	194	15	50	-0.37
7. A1734448-1	192	14	47	-0.40
8. A1978199-4	147	11	47	-0.48
9. A1978199-3	146	10	39	-0.51
10. A1978199-2	146	10	53	-0.51
11. A1734448-3	192	10	42	-0.51
12. A1734448-2	193	10	52	-0.51

1. SEQ-5-2 (1-110)
AI978199_5

```
Initial Score = 109 Optimized Score = 109 Significance = 2.14
Residue Identity = 9% Matches = 109 Mismatches = 1
Gaps = 0 Conservative Substitutions = 0
```

DNLVHPKRGSTALXGHPRLILDDSSMSNELCRILXACQEGNDKRXEFOXVNTRD
 |||||
 HQCCPSRHSVYADDLVLPWPKRGSTALXGHPRLILDDSSMSNELCRILXACQEGNDKRXEFOXVNTRD
 10 x 20 30 40 50 60 70

[illegible]

C1

2: SEQ-5_2 (1-110)
AI734448 4

```
Initial Score = 109 Optimized Score = 109 Significance = 2.14
Residue Identity = 98% Matches = 108 Mismatches = 2
Gaps = 0 Conservative Substitutions = 0
```

	X	10	20	30	40
VARRCGNSDPSLAKDEXDXDDACPSRPTSYVADNDLVHPMKRGSPMALXGRDPPLILDCSSMSNELCRLKACAC	DNLVHPMKRGSTALXGRDPRLIDCSSMSNEICRLKACAC	:	:	:	:
1	2	3	4	5	6
7	8	9	10	11	12
13	14	15	16	17	18
19	20	21	22	23	24
25	26	27	28	29	30

EGNDRKREKPOXVNTBDLAKAVINHAETLEFTEFWYHVAEKQONICLFLLIGITPEGLEMAYTYTLHERS
50 60 70 80 90 100 110

EGNDRKREKPOXVNTBDLAKAVINHAETLEFTEFWYHVAEKQONICLFLLIGITPEGLEMAYTYTLHERSAHA
50 60 70 80 90 100 110 120

GCRHMLELLFCWIGQLPCFVIRRXSIAFLVKPVDNLLXXXXXXXXXXXX
 150 160 170 180 190

3. SEQ-5.2 (1-110)
AT734448_5

Initial Score	=	20	Optimized Score	=	49	Significance	=	-0.24
Residue Identity	=	12%	Matches	=	14	Mismatches	=	92
Gaps	=	0	Conservative Substitutions				=	4

```

X 10 20 30 40
DNLVHPMKRGSTWALXGRDPRLLDCCSSWSNELCRLXACQ
SGGLAIVTPPFDVMMKXRMMPAPPGPVSMOMILLILGNEGPIGLFGAIIPRFWIAPLCAMNFAGYELAK
10 20 30 X 40 50 60 70
EGNDKRXEKQXVNTDLAKKAVINHAFTFLFYFWVHVAEKOONICLFLILGITFPXGLEMAVXYTLHKS
10 20 30 40 50 60 70 80 90 100 110 120 130 140 X
KAMIKDEKNSSESTREILPRKQXSTMQLFFIFGSMLOQRNRTSAFFXWELHSRALRMLYSIHYMKVLE
80 90 100 110 120 130 140 X
DRGWCSCSCFAGXDSLVLLSADDPXPSLLNPMXICSKKKKKKKKK
150 160 170 180 190

4. SEQ-5_2 (1-110)
AI978199_6
Initial Score ~ 18 Optimized Score ~ 49 Significance ~ -0.29
Residue Identity ~ 12% Matches ~ 14 Mismatches ~ 92
Gaps ~ 0 Conservative Substitutions ~ 4

X 10 20 30 40 50
DNLVHPMKRGSTWALXGRDPRLLDCCSSWSNELCRLXACQEGNDKRXEKQXVNTDL
TRTAPRPTPVSMOMILLILGNEGPIGLFGAIIPRFWIAPLCAMNFAGYELAKKAMIKDEKNSSESTREIL
10 X 20 30 40 50 60 70
60 70 80 90 100 110
AKKAVINHAFTFLFYFWVHVAEKOONICLFLILGITFPXGLEMAVXYTLHKS
10 20 30 40 50 60 70 80 90 100 110 120 130 140
PRKQXSTMQLFFIFGSMLOQRNRTSAFFXWELHSRALRMLYSIHYMKVLEDRGTCSCSCFAGXDSLV
80 90 100 110 120 X 130 140

VL

5. SEQ-5_2 (1-110)
AI978199_1 TOIG of: a1978199 check: 48 from: 1 to: 442
Initial Score ~ 15 Optimized Score ~ 50 Significance ~ -0.37
Residue Identity ~ 10% Matches ~ 12 Mismatches ~ 93
Gaps ~ 0 Conservative Substitutions ~ 5

X 10 20 30 40 50 60 70
DNLVHPMKRGSTWALXGRDPRLLDCCSSWSNELCRLXACQEGNDKRXEKQXVNTDLAKKAVINHAFTFL
NKTSELSYPAKEQQLQHVPLSSSTFLMXCILYSHLAKALRECNQOYOKKADVULLLCMDPKIKKXSCMDVHC
X 10 20 30 40 50 60 70
FYFWVHVAEKOONICLFLILGITFPXGLEMAVXYTLHKS
10 20 30 40 50 60 70 80 90 100 110 120 130 140
FLGKISRVDLEFFSSFIILAFKASXPAKFIAPRGAIQKRGIAPLKSPSPPRMDKIIICIDTGVPGGA
80 90 100 110 X 120 130 140

VLV

6. SEQ-5_2 (1-110)
AI734448_1 TOIG of: a1734448 check: 6406 from: 1 to: 582
Initial Score ~ 15 Optimized Score ~ 50 Significance ~ -0.37
Residue Identity ~ 10% Matches ~ 12 Mismatches ~ 93
Gaps ~ 0 Conservative Substitutions ~ 5

X 10 20 30 40
DNLVHPMKRGSTWALXGRDPRLLDCCSSWSNELCRLXACQ
FEFFFEFFLEQIYIGFNKEGYSSADNKTRELTSYPAKEQQLQHVPLSSSTFLMXCILYSHLAKALRECN

```

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10 20 30 X 40 50 60 70
GNDKRXEKQXVNTDLAKKAVINHAFTFLFYFWVHVAEKOONICLFLILGITFPXGLEMAVXYTLHKS
10 20 30 40 50 60 70 80 90 100 X
QYOKKADVULLLCMDPKIKKXSCMDVHCFLGKISRVDLEFFSSFIILAFKASXPAKFIAPRGAIQKRGCI
80 90 100 110 120 130 140
APLKSPPGSPSPPRMDKIIICIDTGVPGAGIILAFITSKGCVTIAS
150 160 170 180 190

7. SEQ-5_2 (1-110)
AI734448_6
Initial Score ~ 14 Optimized Score ~ 47 Significance ~ -0.40
Residue Identity ~ 12% Matches ~ 14 Mismatches ~ 85
Gaps ~ 0 Conservative Substitutions ~ 7

X 10 20 30 40
DNLVHPMKRGSTWALXGRDPRLLDCCSSWSNELCRLXACQ
LEDLRQXXPLPLTFXXLXGCLPLQAHQCLCRXXSCPSELTFRVPLGSLARSPASSGILLLEQXTLQMSLPR
10 20 30 X 40 50 60 70
EGNVRXRXEKQXVNTDLAKKAVINHAFTFLFYFWVHVAEKOONICLFLILGITFPXGLEMAVXYTLHKS
10 20 30 40 50 60 70 80 90 100 110
RQXXKMRKRIEVSQHERSCQSDOPCNFFILFLGPPCCREATEHLPPFDIGNYIPVGXDCDIYITREKQXR
80 90 100 110 120 130 140 X
TEAHAGAVULLDRTAPLFCYPPRIHSLPCXTRCKEFLAKKKKKKKKK
150 160 170 180 190

3. SEQ-5_2 (1-110)
AI978199_4
Initial Score ~ 11 Optimized Score ~ 47 Significance ~ -0.48
Residue Identity ~ 12% Matches ~ 14 Mismatches ~ 89
Gaps ~ 0 Conservative Substitutions ~ 7

X 10 20 30 40 50
DNLVHPMKRGSTWALXGRDPRLLDCCSSWSNELCRLXACQEGNDKRXEKQXVNTDL
APGAPLQAHQCLCRXXSCPSELTFRVPLGSLARSPASSGILLLEQXTLQMSLPRRQXXKMRKRIEVSQHERS
10 X 20 30 40 50 60 70
LAKKAVINHAFTFLFYFWVHVAEKOONICLFLILGITFPXGLEMAVXYTLHKS
10 20 30 40 50 60 70 80 90 100 110 120 130 140
COHSSDOPCNFFILFLGPPCCREATEHLPPFDIGNYIPVGXDCDIYITREKQXRTEAHAGAVULLDRTAH
80 90 100 110 120 X 130 140

LFC

9. SEQ-5_2 (1-110)
AI979199_3
Initial Score ~ 10 Optimized Score ~ 39 Significance ~ -0.51
Residue Identity ~ 11% Matches ~ 11 Mismatches ~ 85
Gaps ~ 0 Conservative Substitutions ~ 2

X 10 20
DNLVHPMKRGSTWALXGRDPRLL
QNKAVIISKRRTTAPACASVLXHFHSHVMTIOPSOCPGKXPPISKKGRCVASIQQHPKNNKIKKLHGXSLL
10 20 30 40 50 60 70 80 90
DCCSWSNELCRLXACQEGNDKRXEKQXVNTDLAKKAVINHAFTFLFYFWVHVAEKOONICLFLILGITFPX

```


X 10 20 30 40 50
XXSCPSLETRVHLGSLRARSPASSGLLLEQXTLQAMSLPRQXXKMRKIPVSC

```

WRITGNSDPSLXREXDXDQACPSRPTSVYADDNLVHPKRGSPMALXGDDPILLDCSSWSNEDLCRLXACC
      10      20      30      40      50      60      70
-----HERSQESSDQPCNFELFLFPGCCRETEHLPEFDDIGNVYIPGXDGCIVYTTXEC
      60      70      80      90     100     110
EGNDKRXEFOXVNTFLDLAKKAVYNHATFLFEPWVHVAEQOQNICFLIGITPFGLEMAVXYLHESAR
      80      90     100     110     120     130     140 X
GGRHLELLFCWIGOLPCFVYIRRXSIAPLVLKDPDVNLXKKKKKKKK
      150     160     170     180     190

```

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Init. Opt.

Sequence Name	Description	Length	Score	Score	Sig.	Frame
1. A5978199.4	translational frame	147	111	111	2.16	0

The list of other best scores is:

Sequence Name	Description	Length	Int. Opt. Score	Sig. Frame
-----	-----	-----	-----	-----

[illegible]

```

1. SEQ-5_1 (1-111)
   A1978199_4
Initial Score = 111 Optimized score = 111 Significance = 2.16
Residue Identity = 100% Matches = 111 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

```

60 70 80 90 100 110
 COSSDOPCNFFILFGLPCCREATEHLPEFPIGNVYIPVPGDGCIVYITXKC
 COSSDOPCNFFILFGLPCCREATEHLPEFPIGNVYIPVPGDGCIVYITXKC
 COSSDOPCNFFILFGLPCCREATEHLPEFPIGNVYIPVPGDGCIVYITXKC
 80 90 100 110 120 130 140
 COSSDOPCNFFILFGLPCCREATEHLPEFPIGNVYIPVPGDGCIVYITXKC
 COSSDOPCNFFILFGLPCCREATEHLPEFPIGNVYIPVPGDGCIVYITXKC
 COSSDOPCNFFILFGLPCCREATEHLPEFPIGNVYIPVPGDGCIVYITXKC

0.57

```

2. SEQ5_1 (1-111)
   A1731448_6
Initial Score      = 110 Optimized score = 110 Significance = 2.13
Residue Identity  = 99% Matches      = 110 Mismatches   = 1
Caps              = 0 Conservative Substitutions = 0

```

[illegible]

3. SEQ-5-1 (1-111)
AT978199_3

Initial Score = 15 Optimized Score = 48 Significance = -0.37
Residue Identity = 11% Matches = 13 Mismatches = 94
Gaps = 0 Conservative Substitutions = 4

10 X 10 20 30 40 50
X X S C P S L E T R V H L G S L R A R S P A S G L L L E O X T L Q A M S L P R R O X X K M R K I P V S Q H E
Q N K X A V L S S K R T T A P A C A S V L M H F S H V M T I O P S G P T G M X F P I S K K G R C S V A S L O H G P R N K I K K L H G X S L L
10 X 20 30 40 50 60 70
X X S C P S L E T R V H L G S L R A R S P A S G L L L E O X T L Q A M S L P R R O X X K M R K I P V S Q H E
R S G Q E S S D Q P C N F F I L G P C C R E A T E H L P F P D I G N Y I P V G P X D G C I V Y I T X E K C X
S M O D L S C X L G I F L I Y H G L L G K L I C K X H C S K R S N P E E A G D R A L E P P K T T L V S K G O D Y H L H R H M C A M G S
80 90 100 110 120 130 140
P G

4. SEQ-5_1 (1-111)
A1734448_3

Initial Score = 15 Optimized Score = 48 Significance = -0.37
Residue Identity = 11% Matches = 13 Mismatches = 94
Gaps = 0 Conservative Substitutions = 4

10 X 10 20
X X S C P S L E T R V H L G S L R A R S P A S G L L
F F F F F F F F F F R A N L H R V X G R L M I G X O N K G A V L S K R T T A P A C A S V L M H F S H V M T I O P S G P T G M X F P
10 20 30 40 50 60 70
L E O X T L Q A M S L P R R O X X K M R K I P V S Q H E R S C Q E S S D Q P C N F F I L G P C C R E A T E H L P F P D I G N Y I P V G P X
I S K K G R C S V A S L O H G P R N K I K K L H G X S L S M O D L S C X L G I F L I Y H G L L G K L I C K X H C S K R S N P E E A G D R
80 90 100 110 120 130 140
100 110
D C G I V Y I T X E K C
A L E P K G T L V S K D G O D Y H L H R H M A M A R G R H H P X L H V K G R G H Y C R K S S
150 X 160 170 180 190

5. SEQ-5_1 (1-111)
A1978199_2

Initial Score = 14 Optimized Score = 43 Significance = -0.40
Residue Identity = 10% Matches = 10 Mismatches = 78
Gaps = 0 Conservative Substitutions = 6

10 X 10 20
X X S C P S L E T R V H L G S L R A R S P A
Q V S C P I O Q K N N S S M C L P A L F S C V N Y T A I S R P G N V I P N I K K R O M E C C S F A T W T O K X N K K V A M L I T A F L
10 20 30 40 50 X 60 70
S S G L L L E O X T L Q A M S L P R R O X X K M R K I P V S Q H E R S C Q E S S D Q P C N F F I L G P C C R E A T E H L P F P D I G N Y I
A R S L V I T H M N F S H L S L P S W O A H S L O S L L Q E O S R R S G S R X R A Q V D R P F G M T R L S A X T L V G L E G O S W
80 90 100 110 120 130 140
100 110
P V G P X D G C I V Y I T X E K C

6. SEQ-5_1 (1-111)
A1734448_5

Initial Score = 14 Optimized Score = 33 Significance = -0.40

Residue Identity = 5% Matches = 5 Mismatches = 77
Gaps = 0 Conservative Substitutions = 3

10 X 10 20
X X S C P S L E T R V H L G S L R A R S P A
P L G A M N F A G E L A K K M I N D E K N S S E S T R E I L P R K O X S T M O L F F I F G S M L O R S N T S A F F X Y W E L H S R A L
60 70 80 90 100 110 120 130
S S G L L L E O X T L Q A M S L P R R O X X K M R K I P V S Q H E R S C Q E S S D Q P C N F F I L G P C C R E A T E H L P F P D I G N Y I
R M L X S H Y M K V L E D R G T C S C C S F A G X D S L V L S A D D P X P S L L P M X I C S K K K K K K K K K K
140 150 160 170 180 190 X
100 110
P V G P X D G C I V Y I T X E K C

7. SEQ-5_1 (1-111)
A1734448_2

Initial Score = 14 Optimized Score = 48 Significance = -0.40
Residue Identity = 9% Matches = 10 Mismatches = 95
Gaps = 0 Conservative Substitutions = 6

10 X 10 20
X X S C P S L E T R V H L G S L R A R S P A
O G S C P I O Q K N N S S M C L P A L F S C V N Y T A I S R P G N V I P N I K K R O M E C C S F A T W T O K X N K K V A M L I T A F L
40 50 60 70 80 X 90 100
S S G L L L E O X T L Q A M S L P R R O X X K M R K I P V S Q H E R S C Q E S S D Q P C N F F I L G P C C R E A T E H L P F P D I G N Y I
A R S L V I T H M N F S H L S L P S W O A H S L O S L L Q E O S R R S G S R X R A Q V D R P F G M T R L S A X T L V G L E G O S
110 120 130 140 150 160 170
100 110
P V G P X D G C I V Y I T X E K C
S X X S R O R E G S L L P O V I Q
180 190 X

8. SEQ-5_1 (1-111)
A1978199_6

Initial Score = 13 Optimized Score = 17 Significance = -0.42
Residue Identity = 12% Matches = 5 Mismatches = 34
Gaps = 0 Conservative Substitutions = 2

10 X 10 20
X X S C P S L E T R V H L G S L R A R S P A
A M I K D E K N S S E S T R E I L P R K O X S T M O L F F I F G S M L O R S N T S A F F X Y W E L H S R A L R M L Y S I H Y R K Y L E D
60 70 80 90 100 X 110 120
S S G L L L E O X T L Q A M S L P R R O X X K M R K I P V S Q H E R S C Q E S S D Q P C N F F I L G P C C R E A T E H L P F P D I G
R G T C W S C C S F A G X D S S L V L
130 140 X

9. SEQ-5_1 (1-111)
A1978199_5

Initial Score = 13 Optimized Score = 49 Significance = -0.42
Residue Identity = 12% Matches = 15 Mismatches = 89
Gaps = 13 Conservative Substitutions = 7

10 X 20 30 40 50

Initial Score = 9 Optimized Score = 37 Significance = -0.47
 Residue Identity = 5% Matches = 5 Mismatches = 75
 Gaps = 0 Conservative Substitutions = 5

10 20 30 40 50 60 70
 HFSHWYTIQPSQPTGMKFPISKRGCSVASLQHPKNIKIKLHGXSLSMODLSXLTGIFLLFYHCLLG
 : : : : : : :
 TKQVSCPIQOKNNSSSMWCLPLAFSCNVYYTAISRPGNVIPNIK
 X 10 20 30 40

80 90 100 110
 KLIACKVHCSKRSNPEAGDRALKPEKWTLVSKDGQDY
 : : : : :
 ROMFCCFSATWTOXKXKKVAVMLITAFILARSILVLTWNFSHLSPSWQAHSLQSEOSRRSGSRPXR
 50 60 70 80 90 100 110

120
 AOVDPFQGWTRLSA
 130

10. SEQ-5_5 (1-110)
 AI734448_4

Initial Score = 9 Optimized Score = 44 Significance = -0.47
 Residue Identity = 9% Matches = 10 Mismatches = 97
 Gaps = 0 Conservative Substitutions = 3

X 10 20 30 40 50 60
 HFSHWYTIQPSQPTGMKFPISKRGCSVASLQHPKNIKIKLHGXSLSMODLSXLTGIFLLF
 : : : : : : :
 VMRTGNSDPSLXRDXXDDACPSRPTSVYADNLVHMKRGSFWALXGRDPLLDSCSWSELCRLXACQ
 X 10 20 30 40 50 60 70

80 90 100 110 120 130 140
 YHCLGKLIACKVHCSKRSNPEAGDRALKPEKWTLVSKDGQDY
 : : : : : : :
 EGNDRKXKXFOXVNTRODLAKKAVINHAATFLFYFWVHAQKQONICLFLITGPXGLEMAVXYTLHEKSAR
 80 90 100 110 120 130 140

GQRHMLLELFCWIGOLPCFYI
 150 160

11. SEQ-5_5 (1-110)
 AI734448_2

Initial Score = 8 Optimized Score = 49 Significance = -0.49
 Residue Identity = 12% Matches = 14 Mismatches = 90
 Gaps = 0 Conservative Substitutions = 6

X 10 20
 HFSHWYTIQPSQPTGMKFP
 : : : : : : :
 TSGLTRKAMDHRITKQSCPIQOKNNSSSMWCLPLAFSCNVYYTAISRPGNVIPNIKROMFCCFSATW
 20 30 40 50 60 70 80

30 40 50 60 70 80 90
 SKKGRCSVASLQHPKNIKIKLHGXSLSMODLSXLTGIFLLFYHCLGKLIACKVHCSKRSNPEAGDRA
 : : : : : : :
 TOKXKKKXVAVMLITAFILARSILVLTWNFSHLSPSWQAHSLQSEOSRRSGSRPXAQGDPRFQGW
 90 100 110 120 130 140 150

100 110
 LKEPKWTLVSKDGQDY
 : : : : :
 RLSAXTLVGLGEGQASSXSSRQREGSILPOVLO
 160 170 X 180 190

12. SEQ-5_5 (1-110)
 AI734448_6

Initial Score = 7 Optimized Score = 46 Significance = -0.52
 Residue Identity = 10% Matches = 11 Mismatches = 94
 Gaps = 0 Conservative Substitutions = 5

X 10 20
 HFSHWYTIQPSQPTGMKFP
 : : : : : : :
 DLRQXXPLPLTXXLXGCLPLQAHQCLCRXXSCPSLETFRVPLGSLRARSPPASSGLLLEQXTLQAMSLPRQ
 10 20 30 40 50 60 70

30 40 50 60 70 80 90
 SKKGRCSVASLQHPKNIKIKLHGXSLSMODLSXLTGIFLLFYHCLGKLIACKVHCSKRSNPEAGDRA
 : : : : : : :
 XXKMRIPVSGHERSCQESSDQPCNFFILFLGPPCCREATHELPFFDIGNYIPVGPXDCIYVITXKXCXTE
 80 90 100 110 120 130 140

100 110
 LKEPKWTLVSKDGQDY
 : : : : :
 AHAGAVLLLDRTAPLFCYPPMIHSLPCXTRCKFALKKKKKKKKK
 150 160 X 170 180 190

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> O <
O I O < Intelligence
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file seq-5_3.res made by bobryen on Thu 28 Feb 102 15:45:52-PSW.

Query sequence being compared: SEQ-5_3 (1-109)
Number of sequences searched: 12
Number of scores above cutoff: 12

Results of the initial comparison of SEQ-5_3 (1-109) with:
File: genbanktrans.pep

Seq 5, translation frame 3

100-
N -
U -
M -
B -
E -
R -
O -
F 10-
S -
E -
U -
Q -
N -
C -
E -
S -
SCORE 0 121 24 36 481 60 72 841 96 108
STDEV 0 1 1 1 1 1 1 1 1 1

PARAMETERS

Similarity matrix PAM-150 K-tuple 1
Threshold level of sim. 16
Mismatch penalty 1 Joining penalty 20
Gap penalty 5.00 Window size 109
Gap size penalty 0.05
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean 31 Median 19 Standard Deviation 35.91
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00
Number of residues: 2036
Number of sequences searched: 12
Number of scores above cutoff: 12

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt.	Sign.	Frame
1. A1978199_6	**** 2 standard deviations above mean ****	146	108	108	2.14	0
2. A1734448_5	**** 0 standard deviation from mean ****	193	108	108	2.14	0
3. A1734448_6		192	22	49	-0.25	0
4. A1978199_4		147	21	48	-0.28	0
5. A1978199_5		146	19	47	-0.33	0
6. A1734448_4		194	19	48	-0.33	0
7. A1978199_1	TOIG of: a1978199 check: 48	147	18	37	-0.36	0
8. A1734448_1	TOIG of: a1734448 check: 640	194	18	44	-0.36	0
9. A1978199_2		146	13	49	-0.50	0
10. A1978199_3		146	11	52	-0.56	0
11. A1734448_3		192	11	52	-0.56	0
12. A1734448_2		193	11	49	-0.56	0

1. SEQ-5_3 (1-109)
A1978199_6
Initial Score = 108 Optimized Score = 108 Significance = 2.14
Residue Identity = 99% Matches = 108 Mismatches = 1
Gaps = 0 Conservative Substitutions = 0

60 70 80 90 100 110 120 130 140
PRKXSTNQLFFIFGSMLOSRNRTSAFFXYWELHSRRALRWLYSIHYMRK
PRKXSTNQLFFIFGSMLOSRNRTSAFFXYWELHSRRALRWLYSIHYMRK
PRKXSTNQLFFIFGSMLOSRNRTSAFFXYWELHSRRALRWLYSIHYMRK
80 90 100 110 120 130 140
VL

2. SEQ-5_3 (1-109)
A1734448_5
Initial Score = 108 Optimized Score = 108 Significance = 2.14
Residue Identity = 99% Matches = 108 Mismatches = 1
Gaps = 0 Conservative Substitutions = 0

SGGLAIVTPPPDVMKXRMPPAPCPBPVSMOMITLILGNEGPLGLEKAIPIFFWIAPLGAMNFAGYELAK
10 20 30 40 50 60 70
KAWIDKXSSSESTREILPRKXSTNQLFFIFGSMLOSRNRTSAFFXYWELHSRRALRWLYSIHYMRK
KAWIDKXSSSESTREILPRKXSTNQLFFIFGSMLOSRNRTSAFFXYWELHSRRALRWLYSIHYMRK
80 90 100 110 120 130 140
CGTCMCCSCFAGXDSIVLISADDPXPSSLNPMXICSKKKKKKKK

3. SEQ-5_3 (1-109)
A1734448_6
Initial Score = 22 Optimized Score = 49 Significance = -0.25
Residue Identity = 108 Matches = 16 Mismatches = 83
Gaps = 44 Conservative Substitutions = 10

```

111LILSLGNEGPLGLFKGAIPGFFWIIAPLPGANNFAGYELH
WMRTICGNSDPSLKHDEXXDDACPSRPTSVIYADDNLVHPMKGSPFALKGRDPLLDDCSSVSNELCRHXACQ
10 20 30 40 50 60 70
40 50 60 70 80 90 100
KKAKIKDEKNSSESTREILPFRKQKSTWQLFYEFIFGSMLOBSNRTSAFFXYWELHSRRLRWLYSIHYMRK
EGNDRKRKEKQXVNTROLAKAVINHATFLEFYFWYHVAEKOQNICLEFELIGITTPPXGLEMAVXYTLHEKSRNR
80 90 100 110 120 130 140 X
GQRHMLELLEPCWIGOLPCFVIRRXSIAFLVYKPDVNLKXKKKKKKK
150 160 170 180 190
9. SEO-5.3 (1-109)
AI978199_1 TOIG of: a1978199 check: 48 from: 1 to: 442
Initial Score ~ 18 Optimized Score ~ 37 Significance ~ -0.36
Residue Identity ~ 4% Matches ~ 4 Mismatches ~ 75
Caps ~ 0 Conservative Substitutions ~ 5
X 10 20
111LILSLGNEGPLGLFKGAIPGFFWIIAPLPGANNFAGYELH
OLQHVPLSSSTFLMXCILYSHLALRECNOSYORKADVLLLLCNMDPKIKKXSCWVDCFLGISRVDSLEFPE
20 30 40 50 60 70 80 90
30 40 50 60 70 80 90
FWIAPLPGANNFAGYELKAKKAMIKDEKNSSESTREILPFRKQKSTWQLFYEFIFGSMLOBSNRTSAFFXYWELHS
1 FSSIIIAFLASSXPAKFIAPRCAGIQRKGIAPLPSGSPSPRMDKIIICIDTGGVPGGAVLV
90 100 110 120 130 140 X
100
RRFARMLYSIHMYRK
8. SEO-5.3 (1-109)
AI734448_1 TOIG of: a1734448 check: 6406 from: 1 to: 582
Initial Score ~ 18 Optimized Score ~ 44 Significance ~ -0.36
Residue Identity ~ 11% Matches ~ 11 Mismatches ~ 77
Caps ~ 0 Conservative Substitutions ~ 6
X 10 20
111LILSLGNEGPLGLFKGAIPGFFWIIAPLPGANNFAGYELH
SSRFELMXCILYSHLALRECNOSYORKADVLLLLCNMDPKIKKXSCWVDCFLGISRVDSLEFPESSFTIA
60 70 80 90 100 110 120
30 40 50 60 70 80 90 X
FWIAPLPGANNFAGYELKAKKAMIKDEKNSSESTREILPFRKQKSTWQLFYEFIFGSMLOBSNRTSAFFXYWELHS
LASXPAKFIAPRCAGIQRKGIAPLPSGSPSPRMDKIIICIDTGGVPGGAVLV
130 140 150 160 170 180 190 X
100
RKALRWLYSIHYMRK
9. SEO-5.3 (1-109)
AI978199_2
Initial Score ~ 13 Optimized Score ~ 49 Significance ~ -0.50
Residue Identity ~ 10% Matches ~ 11 Mismatches ~ 87
Caps ~ 0 Conservative Substitutions ~ 11
X 10 20 30 40 50
111LILSLGNEGPLGLFKGAIPGFFWIIAPLPGANNFAGYELKAKKAMIKDEKNSSESTREI
TKGVSCPLOOKNNNSMCLGCLAFSCNVVYTAISRPGVNIPIMKRQWPCFSATWTQKXNKKVAVLITPA
10 20 30 40 50 60 70

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; Entered [bobyen 28-Feb-02 15:41]

SEQ-5_1
XXCPSLETRVHLSLRARSPASSGLLEOXTLOAMSLPRROXKKMRKIPVSOHERSCOESSDOPCNFF
ILFLGPCREATEHLPPFDIGNYIPVGPYDGCIVITIXECI

SEQ-5_2
DNLVHFMKRGSTWALXGRDPRLLDCSSNSNEICRLACOEGRDNRKXKFOXYNTDOLAKKAVINHATEL
FYFWHVAERQONICLFLILGITFPYGLEMAVYTTLHEKSI

SEQ-5_3
ILSTIGNECPGLIFKGAIPGFPIAPLGAMNFAGYELAKKAMI KDEKNSESTREILPRKXSTWOLFV
FITGSMLOQRNRTSAFFPYWELHSRRLRWLYSIHIMRKI

SEQ-5_4
ALFSCNVYVTAISRPGNVI PNIRKROMFCCFSATWOKXKKVAVMLITAFARSLVLTWNFSHLISLP
SMOAHSLQSSLLQEQSRRSRGRSPXRAQVDPFRQGWTRLSI

SEQ-5_5
HESHVITTTOPSGOPTGMXFPISKKGRCVASLQHGPKNKIKKLHGXSLSMODLSCXLTGITFLIFYHCL
LGKLIACKVHCSKRSNPEEGDRALKEPKWTLVSKDGDYI

SEQ-5_6
TFLMXCILYSHLALRECNQYOKKADVILLLCNMDPKIKXKSCWVDHCFLGKISRVDLSEFFSFIIAF
LASSYPAKFTIAPRGAIQKKGINPLKSPSGPSFPRMDKI

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RESULTS: 1
LOCUS: AI978199/c
DEFINITION: 614041D10.x2 614 - root cDNA library from Walbot Lab: Zea mays cDNA, mRNA sequence.
ACCESSION: AI978199
VERSION: AI978199.1 GI:5791407
KEYWORDS: EST.
SOURCE: Zea mays.
ORGANISM: Zea mays
DE: Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae
CA: Andropogoneae; Zea.
REFERENCE: 1 (bases 1 to 442)
DE: Walbot, V.
BY: Maize ESTs from various cDNA libraries sequenced at Stanford University
TITLE: University
JOURNAL: Unpublished (1999)
COMMENT: Contact: Walbot V
CA: Department of Biological Sciences
DE: Stanford University
CA: 855 California Ave, Palo Alto, CA 94304, USA
DE: Tel: 650 723 2227
CA: Fax: 650 725 8221
DE: Email: walbot@stanford.edu
CA: Plate: 614041 row: D column: 10.
FEATURES:
source
 Location/Qualifiers
 1..442
 /organism="Zea mays"
 /cultivar="W23"
 /db_xref="taxon:4577"
 /clone_lib="614 - root cDNA library from Walbot Lab"
 /tissue_type="root"
 /dev_stage="3-4 days old"
 /lab_host="XL0LR"
 /note="Organ: root; Vector: pBlueScriptII SK+; Site_1: EcoRI; Site_2: XhoI; 3-4 days old root tissue from Walbot Lab (LM)"
BASE COUNT 126 a 107 c 93 g 116 t
ORIGIN

Query Match 99.5%; Score 331.4; DB 104; Length 442;
 Best Local Similarity 99.7%; Pred. No. 5e-85;
 Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY      1 tgataatcttgtccatccttggaaacgaggggtccacttgggctctttaagggcgcgatcc 60
Db      400 TGATAATCTTGTCCATCCTTGGAAACGAGGGTCCACTTGGGCTCTTTAAGGGCGCGATCC 341
QY      61 ccccttcttcttgattgctcctcttggagcaatgaactttgcaggctatgagcttgcca 120
Db      340 CCCCTTCTTCTTGATTGCTCCTCTTGGAGCAATGAACCTTGCAGGCTATGAGCTTGCCA 281
QY      121 agaaggcaatgataaaagatgagaaaaattccagtgagtcaacacgagagatcttgccaa 180
Db      280 AGAAGGCAATGATAAAAGATGAGAAAAATTCCAGTGAGTCAACACGAGAGATCTTGCCAA 221
QY      181 gaaagcagtgatcaaccatgcaactttttttattttttgggtccatgttgagagaa 240
Db      220 GAAAGCAGTGATCAACCATGCAACTTTTTTATTTTATTTTGGGTCCATGTTGAGAGAA 161
QY      241 gcaacagaaacatctgccttttttgatattgggaattacattcccgtagggccttgagat 300
Db      160 GCAACAGAACATCTGCCTTTTTTGTATATTGGGAATTACATTCCCGTAGGGCCTTGAGAT 101
QY      301 ggctgtatagtatacattacatgagaaaagtgc 333
Db      100 GGCTGTATAGTATACATTACATGAGAAAAGTGC 68
  
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Alanine	ala	A	G C N
cysteine	cys	C	U G U U G C
Aspartic Acid	Asp	D	G A U G A C
Glutamic acid	Glu	E	G A A G A G
Phenylalanine	phe	F	U U U U U C
Glycine	gly	G	G G N
Histidine	his	H	C A U C A C
isoleucine	Ile	I	A A U A U C A U A
Lysine	lys	K	A A A A A G
leucine	leu	L	U U U U U G C U N
Methionine	met	M	A U G
Asparagine	asn	N	A A U A A C
Proline	pro	P	C C N
Glutamine	gln	Q	C C A C A G
Arginine	arg	R	C G N A G A A G G
serine	ser	S	U C N A G U A G C
Threonine	thr	T	C A N
valine	val	V	G U N
Tryptophan	trp	W	U G G
Tyrosine	tyr	Y	U A U U A C
STOP			U A A U A G U G A
START			A U G

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AI734448/c
LOCUS AI734448 582 bp mRNA EST 02-FEB-2000
DEFINITION 606031E07.x1 606 - Ear tissue cDNA library from Schmidt lab Zea mays cDNA, mRNA sequence.
ACCESSION AI734448
VERSION AI734448.1 GI:5055561
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 582)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 606031 row: E column: 07.
FEATURES
source Location/Qualifiers
1. 582
/organism="Zea mays"
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/db_xref="taxon:4577"
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/lab_host="XLOLR (Stratagene)"
/note="Organ: immature ear; Vector: pBK-CMV; Site_1: EcoRI
; Site_2: XhoI; Mixed ear tissue cDNA library from Schmidt lab"
BASE COUNT 158 a 131 c 122 g 170 t 1 others
ORIGIN

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Query Match          99.0%; Score 329.8; DB 24; Length 582;
Best Local Similarity 99.4%; Pred. No. 1.5e-84;
Matches 331; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db      487  TGATAATCTTGTCCATCCTTGGAAACGAGGGTCCCTTGGGCTCTTTAAGGCGCGATCC 428

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Qy      121  agaaggcaatgataaaagatgagaaaaattccagtgaagcaacgagagatcttgccaa 180
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Qy      301  ggctgtatagatatacattacatgagaaaagtgc 333
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